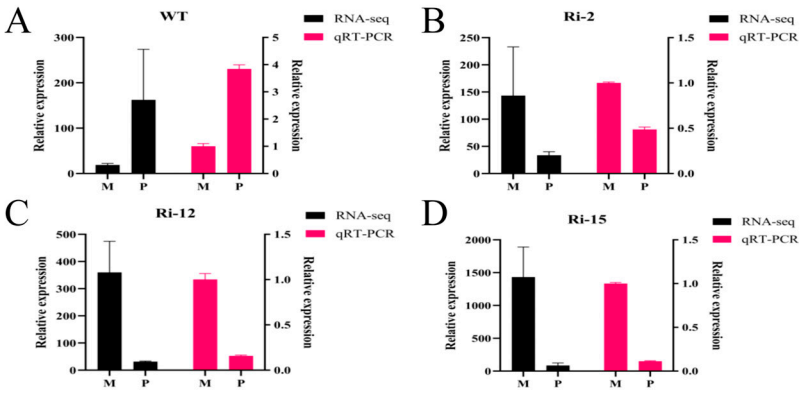

Figure S1. *PoMCA*1 expression between wild type and *PoZCP*26 RNAi strains from mycelia (M) to primordium (P) stage. Black: RNA-seq; Red: qRT-PCR.

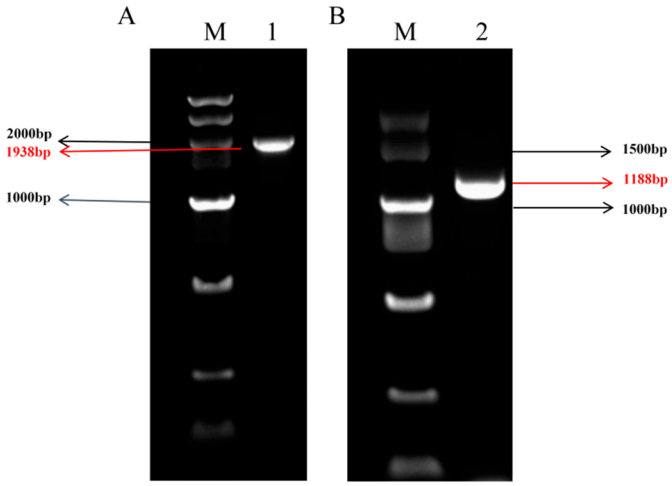

Figure S2. PCR amplification of *PoMCA*1 DNA and CDS. A: DNA, B: CDS. M: Vazyme Marker DL5000bp; 1: DNA 1938 bp; 2: CDS 1188bp.

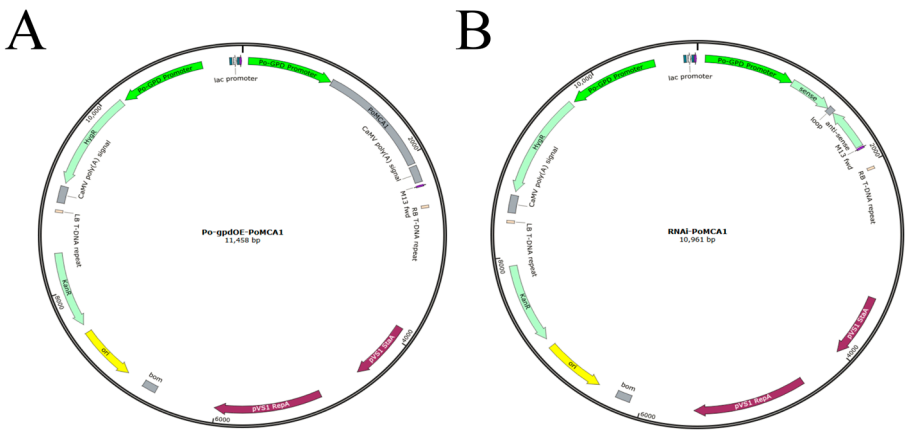

Figure S3. The plasmid maps. A: Po-gpdOE-PoMCA1. B: RNAi-PoMCA1.

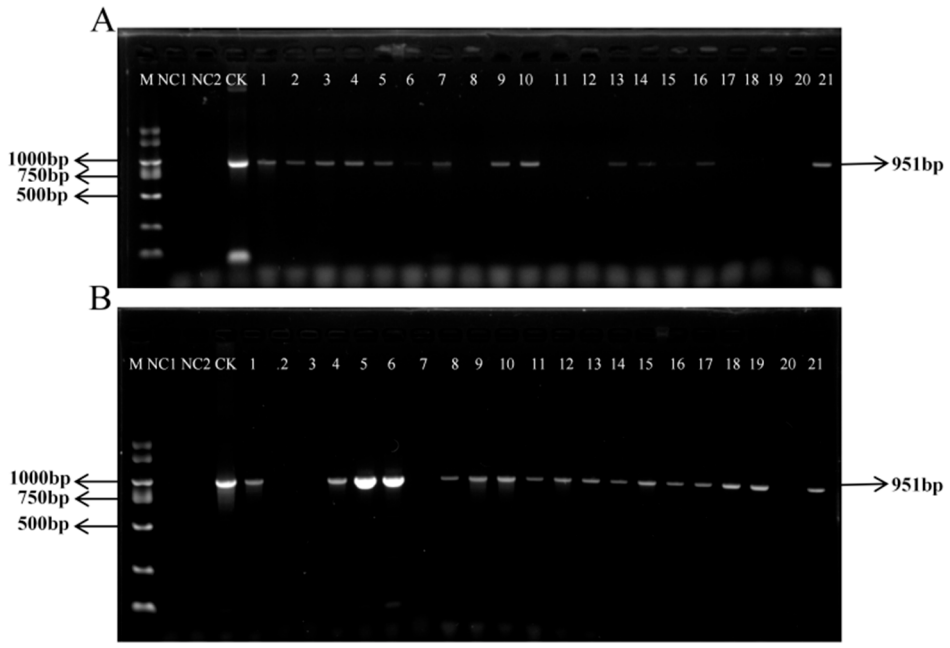

Figure S4. PCR amplification of the hygromycin B phosphotransferase fragment from genome DNA of putative transformants. A: Overexpression, B: RNAi; M: Vazyme Maker DL2000; Lane 1-21: Putative *PoMCA*1 transformants; CK: Positive control (*PoMCA*1 overexpression/RNAi plasmid); NC1: Negative control (wild-type); NC2: Negative control (ddH_2O).

Figure S5. The phenotype of the fruiting bodies of wild type strains and transformants at the 28th day (from the time of inoculation).

Table S1. List of primers in this study.

Primer name	Sequence (5′-3′)
PoMCA1-F	ATGTGCTCTTCTGTCCCCAA
PoMCA1-R	TCACAGACTAAGCTTGTGGT
OE-PoMCA1 F	ACTGACCTGGGGATCCATGTGCTCTTCTGTCCCCAACG
OE-PoMCA1 R	GCATGCCAATTCTAGATCACAGACTAAGCTTGTGGTTGGG
Ri-sense-PoMCA1 F	ACTGACCTGGGGATCCGAACGATGCTTTGAAAATGAAGA
Ri-sense-PoMCA1 R	GCATGCCAATTCTAGACTAGGGGCCGTTTGAGGTC
Ri-anti-PoMCA1 F	CGGCCCCTAGTCTAGACGAAAACGAGTTTGGTATTGGA
Ri-anti-PoMCA1 R	GGCCAGTGCCAAGCTTGAACGATGCTTTGAAAATGAAGA
Hyg-F	CGACAGATCCGGTCGGCATCTACTCTATTTCTT
Hyg-R	TCTCGTGCTTTCAGCTTCGATGTAGGAGGG
qPoMCA1-F (For qRT-PCR)	CCAATCCCAATCCTTCCCTC
qPoMCA1-R (For qRT-PCR)	CATTCAAACCGAGCCCATTC

tub-F (Reference for qRT-PCR)	AGGCTTTCTTGCATTGGTACACGC
tub-R (Reference for qRT-PCR)	TATTCGCCTTCTTCCTCATCGGCA

The underlined letters denoted restriction enzyme cutting sites.